



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) INVENTOR: Adams, Thomas R. et al.
- (ii) TITLE OF INVENTION: Methods and Compositions for the Production of Stably Transformed, Fertile Monocot Plants and Cells Thereof
- (iii) NUMBER OF SEQUENCES: 26
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Arnold, White & Durkee
 - (B) STREET: P.O. Box 4433
 - (C) CITY: Houston
 - (D) STATE: Texas
 - (E) COUNTRY: USA
 - (F) ZIP: 77210
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
 - (D) SOFTWARE: Patent In Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/113,561
 - (B) FILING DATE: 25-AUG-1993
 - (C) CLASSIFICATION: Unknown
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/565,844
 - (B) FILING DATE: 09-AUG-1990
 - (C) CLASSIFICATION: Unknown
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Parker, David L.
 - (B) REGISTRATION NUMBER: 32,165
 - (C) REFERENCE/DOCKET NUMBER: DEKM:055/PAR
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 512/418-3000
 - (B) TELEFAX: 713/789-2679
 - (C) TELEX: 79-0924

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acid residues
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Ala	Thr	Val	Pro	Glu	Leu	Asn	Cys	Glu	Met	Pro	Pro	Ser	Asp
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAGGATCCGT CGACATGGTA AGCTTAGCGG GCCCC

35

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GATCCGTCGA CCATGGCGCT TCAAGCTTC

29

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCAGCTGGTA CCGCGAAGTT CGAAGGGCT

29

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTAGACAACA AAGCAGCAAC CATGGCCAGC ATGCAAGGCC TCATGCATC

49

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGGGATGCA TGAGGCCTTG CATGCTGGCC ATGGTTGCTG CTTTGTGT

49

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acid residues
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Ser Met Gln Gly Leu Met His Pro Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acid residues
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Val Lys Cys Met Gln Val
1 5

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAGUGAAGUG AAGUGAAG

18

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1845 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..1839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG GAT AAC AAT CCG AAC ATC AAT GAA TGC ATT CCT TAC AAT TGC CTC	48
Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu	
1 5 10 15	
AGC AAC CCT GAA GTG GAA GTG CTG GGT GGC GAA CGC ATC GAA ACC GGT	96
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly	
20 25 30	
TAC ACC CCA ATC GAT ATT TCC CTG TCC CTG ACC CAA TTT CTG CTG AGC	144
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser	
35 40 45	
GAA TTT GTG CCC GGT GCT GGC TTT GTG CTG GGC CTG GTG GAT ATC ATC	192
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile	
50 55 60	
TGG GGC ATT TTT GGT CCC TCC CAA TGG GAC GCC TTT CTG GTG CAA ATT	240
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile	
65 70 75 80	
GAA CAG CTG ATT AAC CAA CGC ATC GAA GAA TTC GCT AGG AAC CAA GCC	288
Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala	
85 90 95	
ATT TCC CGC CTG GAA GGC CTG AGC AAT CTG TAC CAA ATT TAC GCC GAA	336
Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu	
100 105 110	
TCC TTT CGC GAG TGG GAA GCC GAT CCT ACC AAT CCA GCC CTG CGC GAA	384
Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu	
115 120 125	
GAG ATG CGC ATT CAA TTC AAT GAC ATG AAC AGC GCC CTG ACC ACC GCT	432
Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala	
130 135 140	
ATT CCT CTG TTT GCC GTG CAA AAT TAC CAA GTG CCT CTG CTG TCC GTG	480
Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val	
145 150 155 160	
TAC GTG CAA GCT GCC AAT CTG CAT CTG TCC GTG CTG CGC GAT GTG TCC	528
Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser	
165 170 175	
GTG TTT GGC CAA AGG TGG GGC TTT GAT GCC GCC ACC ATC AAT AGC CGC	576
Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg	
180 185 190	
TAC AAT GAT CTG ACC AGG CTG ATT GGC AAC TAC ACC GAT TAC GCT GTG	624
Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val	
195 200 205	
CGC TGG TAC AAT ACC GGC CTG GAA CGC GTG TGG GGC CCA GAT TCC CGC	672
Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg	
210 215 220	
GAT TGG GTG AGG TAC AAT CAA TTT CGC CGC GAA CTG ACC CTG ACC GTG	720
Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val	
225 230 235 240	

CTC	GAT	ATC	GTG	GCT	CTG	TTC	CCA	AAT	TAC	GAT	AGC	CGC	CGC	TAC	CCA	768
Leu	Asp	Ile	Val	Ala	Leu	Phe	Pro	Asn	Tyr	Asp	Ser	Arg	Arg	Tyr	Pro	
			245						250					255		
ATT	CGA	ACC	GTG	TCC	CAA	CTG	ACC	CGC	GAA	ATT	TAC	ACC	AAC	CCA	GTG	816
Ile	Arg	Thr	Val	Ser	Gln	Leu	Thr	Arg	Glu	Ile	Tyr	Thr	Asn	Pro	Val	
			260					265					270			
CTG	GAA	AAT	TTT	GAT	GGT	AGC	TTT	CGC	GGC	TCC	GCT	CAG	GGC	ATC	GAA	864
Leu	Glu	Asn	Phe	Asp	Gly	Ser	Phe	Arg	Gly	Ser	Ala	Gln	Gly	Ile	Glu	
		275					280					285				
CGC	AGC	ATT	AGG	AGC	CCA	CAT	CTG	ATG	GAT	ATC	CTG	AAC	AGC	ATC	ACC	912
Arg	Ser	Ile	Arg	Ser	Pro	His	Leu	Met	Asp	Ile	Leu	Asn	Ser	Ile	Thr	
	290					295					300					
ATC	TAC	ACC	GAT	GCT	CAT	AGG	GGT	TAC	TAC	TAC	TGG	TCC	GGC	CAT	CAA	960
Ile	Tyr	Thr	Asp	Ala	His	Arg	Gly	Tyr	Tyr	Tyr	Trp	Ser	Gly	His	Gln	
305					310					315					320	
ATC	ATG	GCT	TCC	CCT	GTG	GGC	TTT	TCC	GGG	CCA	GAA	TTC	ACC	TTT	CCA	1008
Ile	Met	Ala	Ser	Pro	Val	Gly	Phe	Ser	Gly	Pro	Glu	Phe	Thr	Phe	Pro	
				325					330					335		
CTG	TAC	GGC	ACG	ATG	GGC	AAT	GCC	GCT	CCA	CAA	CAA	CGC	ATT	GTG	GCT	1056
Leu	Tyr	Gly	Thr	Met	Gly	Asn	Ala	Ala	Pro	Gln	Gln	Arg	Ile	Val	Ala	
			340					345					350			
CAA	CTG	GGT	CAG	GGC	GTG	TAC	CGC	ACC	CTG	TCC	TCC	ACC	CTG	TAC	CGC	1104
Gln	Leu	Gly	Gln	Gly	Val	Tyr	Arg	Thr	Leu	Ser	Ser	Thr	Leu	Tyr	Arg	
		355					360					365				
CGC	CCT	TTT	AAT	ATC	GGC	ATC	AAC	AAC	CAG	CAA	CTG	TCC	GTG	CTG	GAC	1152
Arg	Pro	Phe	Asn	Ile	Gly	Ile	Asn	Asn	Gln	Gln	Leu	Ser	Val	Leu	Asp	
	370					375					380					
GGC	ACC	GAA	TTT	GCT	TAC	GGC	ACC	TCC	TCC	AAT	CTG	CCA	TCC	GCT	GTA	1200
Gly	Thr	Glu	Phe	Ala	Tyr	Gly	Thr	Ser	Ser	Asn	Leu	Pro	Ser	Ala	Val	
385					390					395					400	
TAC	CGC	AAG	AGC	GGC	ACC	GTG	GAT	TCC	CTG	GAT	GAA	ATC	CCA	CCA	CAG	1248
Tyr	Arg	Lys	Ser	Gly	Thr	Val	Asp	Ser	Leu	Asp	Glu	Ile	Pro	Pro	Gln	
			405					410					415			
AAT	AAC	AAC	GTG	CCA	CCT	AGG	CAA	GGC	TTT	AGC	CAT	CGC	CTG	AGC	CAT	1296
Asn	Asn	Asn	Val	Pro	Pro	Arg	Gln	Gly	Phe	Ser	His	Arg	Leu	Ser	His	
			420					425					430			
GTG	TCC	ATG	TTT	CGC	TCC	GGC	TTT	AGC	AAT	AGC	AGC	GTG	AGC	ATC	ATC	1344
Val	Ser	Met	Phe	Arg	Ser	Gly	Phe	Ser	Asn	Ser	Ser	Val	Ser	Ile	Ile	
			435				440					445				
CGC	GCT	CCT	ATG	TTC	TCC	TGG	ATC	CAT	CGC	AGC	GCT	GAA	TTT	AAC	AAC	1392
Arg	Ala	Pro	Met	Phe	Ser	Trp	Ile	His	Arg	Ser	Ala	Glu	Phe	Asn	Asn	
	450					455					460					
ATC	ATT	GCC	TCC	GAT	AGC	ATT	ACC	CAA	ATC	CCT	GCC	GTG	AAG	GGC	AAC	1440
Ile	Ile	Ala	Ser	Asp	Ser	Ile	Thr	Gln	Ile	Pro	Ala	Val	Lys	Gly	Asn	
465					470					475					480	

TTT CTG TTT AAT GGT TCC GTG ATT TCC GGC CCA GGC TTT ACC GGT GGC Phe Leu Phe Asn Gly Ser Val Ile Ser Gly Pro Gly Phe Thr Gly Gly 485 490 495	1488
GAC CTG GTG CGC CTG AAT AGC AGC GGC AAT AAC ATT CAG AAT CGC GGC Asp Leu Val Arg Leu Asn Ser Ser Gly Asn Asn Ile Gln Asn Arg Gly 500 505 510	1536
TAC ATT GAA GTG CCA ATT CAC TTC CCA TCC ACC TCC ACC CGC TAC CGC Tyr Ile Glu Val Pro Ile His Phe Pro Ser Thr Ser Thr Arg Tyr Arg 515 520 525	1584
GTG CGC GTG CGC TAC GCT TCC GTG ACC CCA ATT CAC CTC AAC GTT AAC Val Arg Val Arg Tyr Ala Ser Val Thr Pro Ile His Leu Asn Val Asn 530 535 540	1632
TGG GGC AAT TCC TCC ATT TTT TCC AAT ACC GTG CCA GCT ACC GCT ACC Trp Gly Asn Ser Ser Ile Phe Ser Asn Thr Val Pro Ala Thr Ala Thr 545 550 555 560	1680
TCC CTG GAT AAT CTG CAA TCC AGC GAT TTT GGT TAC TTT GAA AGC GCC Ser Leu Asp Asn Leu Gln Ser Ser Asp Phe Gly Tyr Phe Glu Ser Ala 565 570 575	1728
AAT GCT TTT ACC TCC TCC CTG GGT AAT ATC GTG GGT GTG CGC AAT TTT Asn Ala Phe Thr Ser Ser Leu Gly Asn Ile Val Gly Val Arg Asn Phe 580 585 590	1776
AGC GGC ACC GCC GGC GTG ATC ATC GAC CGC TTT GAA TTT ATT CCA GTG Ser Gly Thr Ala Gly Val Ile Ile Asp Arg Phe Glu Phe Ile Pro Val 595 600 605	1824
ACC GCC ACC CTC GAG TAGGTA Thr Ala Thr Leu Glu 610	1845

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 613 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu 1 5 10 15
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly 20 25 30
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 35 40 45
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 50 55 60
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 65 70 75 80

Glu	Gln	Leu	Ile	Asn	Gln	Arg	Ile	Glu	Glu	Phe	Ala	Arg	Asn	Gln	Ala	
				85					90					95		
Ile	Ser	Arg	Leu	Glu	Gly	Leu	Ser	Asn	Leu	Tyr	Gln	Ile	Tyr	Ala	Glu	
			100					105					110			
Ser	Phe	Arg	Glu	Trp	Glu	Ala	Asp	Pro	Thr	Asn	Pro	Ala	Leu	Arg	Glu	
		115					120					125				
Glu	Met	Arg	Ile	Gln	Phe	Asn	Asp	Met	Asn	Ser	Ala	Leu	Thr	Thr	Ala	
	130					135					140					
Ile	Pro	Leu	Phe	Ala	Val	Gln	Asn	Tyr	Gln	Val	Pro	Leu	Leu	Ser	Val	
145					150					155					160	
Tyr	Val	Gln	Ala	Ala	Asn	Leu	His	Leu	Ser	Val	Leu	Arg	Asp	Val	Ser	
				165					170					175		
Val	Phe	Gly	Gln	Arg	Trp	Gly	Phe	Asp	Ala	Ala	Thr	Ile	Asn	Ser	Arg	
			180					185						190		
Tyr	Asn	Asp	Leu	Thr	Arg	Leu	Ile	Gly	Asn	Tyr	Thr	Asp	Tyr	Ala	Val	
		195					200					205				
Arg	Trp	Tyr	Asn	Thr	Gly	Leu	Glu	Arg	Val	Trp	Gly	Pro	Asp	Ser	Arg	
	210					215					220					
Asp	Trp	Val	Arg	Tyr	Asn	Gln	Phe	Arg	Arg	Glu	Leu	Thr	Leu	Thr	Val	
225					230					235					240	
Leu	Asp	Ile	Val	Ala	Leu	Phe	Pro	Asn	Tyr	Asp	Ser	Arg	Arg	Tyr	Pro	
				245					250					255		
Ile	Arg	Thr	Val	Ser	Gln	Leu	Thr	Arg	Glu	Ile	Tyr	Thr	Asn	Pro	Val	
			260					265						270		
Leu	Glu	Asn	Phe	Asp	Gly	Ser	Phe	Arg	Gly	Ser	Ala	Gln	Gly	Ile	Glu	
		275					280					285				
Arg	Ser	Ile	Arg	Ser	Pro	His	Leu	Met	Asp	Ile	Leu	Asn	Ser	Ile	Thr	
		290				295					300					
Ile	Tyr	Thr	Asp	Ala	His	Arg	Gly	Tyr	Tyr	Tyr	Trp	Ser	Gly	His	Gln	
305					310					315					320	
Ile	Met	Ala	Ser	Pro	Val	Gly	Phe	Ser	Gly	Pro	Glu	Phe	Thr	Phe	Pro	
				325					330					335		
Leu	Tyr	Gly	Thr	Met	Gly	Asn	Ala	Ala	Pro	Gln	Gln	Arg	Ile	Val	Ala	
			340					345						350		
Gln	Leu	Gly	Gln	Gly	Val	Tyr	Arg	Thr	Leu	Ser	Ser	Thr	Leu	Tyr	Arg	
		355					360					365				
Arg	Pro	Phe	Asn	Ile	Gly	Ile	Asn	Asn	Gln	Gln	Leu	Ser	Val	Leu	Asp	
	370					375						380				
Gly	Thr	Glu	Phe	Ala	Tyr	Gly	Thr	Ser	Ser	Asn	Leu	Pro	Ser	Ala	Val	
385					390					395					400	
Tyr	Arg	Lys	Ser	Gly	Thr	Val	Asp	Ser	Leu	Asp	Glu	Ile	Pro	Pro	Gln	
				405					410					415		

Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
 420 425 430
 Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
 435 440 445
 Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
 450 455 460
 Ile Ile Ala Ser Asp Ser Ile Thr Gln Ile Pro Ala Val Lys Gly Asn
 465 470 475 480
 Phe Leu Phe Asn Gly Ser Val Ile Ser Gly Pro Gly Phe Thr Gly Gly
 485 490 495
 Asp Leu Val Arg Leu Asn Ser Ser Gly Asn Asn Ile Gln Asn Arg Gly
 500 505 510
 Tyr Ile Glu Val Pro Ile His Phe Pro Ser Thr Ser Thr Arg Tyr Arg
 515 520 525
 Val Arg Val Arg Tyr Ala Ser Val Thr Pro Ile His Leu Asn Val Asn
 530 535 540
 Trp Gly Asn Ser Ser Ile Phe Ser Asn Thr Val Pro Ala Thr Ala Thr
 545 550 555 560
 Ser Leu Asp Asn Leu Gln Ser Ser Asp Phe Gly Tyr Phe Glu Ser Ala
 565 570 575
 Asn Ala Phe Thr Ser Ser Leu Gly Asn Ile Val Gly Val Arg Asn Phe
 580 585 590
 Ser Gly Thr Ala Gly Val Ile Ile Asp Arg Phe Glu Phe Ile Pro Val
 595 600 605
 Thr Ala Thr Leu Glu
 610

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1848 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG GAT AAC AAT CCG AAC ATC AAT GAA TGC ATT CCT TAC AAT TGC CTC
 Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
 1 5 10 15

48

AGC AAC CCT GAA GTG GAA GTG CTG GGT GGC GAA CGC ATC GAA ACC GGT Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly 20 25 30	96
TAC ACC CCA ATC GAT ATT TCC CTG TCC CTG ACC CAA TTT CTG CTG AGC Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 35 40 45	144
GAA TTT GTG CCC GGT GCT GGC TTT GTG CTG GGC CTG GTG GAT ATC ATC Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 50 55 60	192
TGG GGC ATT TTT GGT CCC TCC CAA TGG GAC GCC TTT CTG GTG CAA ATT Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 65 70 75 80	240
GAA CAG CTG ATT AAC CAA CGC ATC GAA GAA TTC GCT AGG AAC CAA GCC Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 85 90 95	288
ATT TCC CGC CTG GAA GGC CTG AGC AAT CTG TAC CAA ATT TAC GCC GAA Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 100 105 110	336
TCC TTT CGC GAG TGG GAA GCC GAT CCT ACC AAT CCA GCC CTG CGC GAA Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 115 120 125	384
GAG ATG CGC ATT CAA TTC AAT GAC ATG AAC AGC GCC CTG ACC ACC GCT Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 130 135 140	432
ATT CCT CTG TTT GCC GTG CAA AAT TAC CAA GTG CCT CTG CTG TCC GTG Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 145 150 155 160	480
TAC GTG CAA GCT GCC AAT CTG CAT CTG TCC GTG CTG CGC GAT GTG TCC Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 165 170 175	528
GTG TTT GGC CAA AGG TGG GGC TTT GAT GCC GCC ACC ATC AAT AGC CGC Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 180 185 190	576
TAC AAT GAT CTG ACC AGG CTG ATT GGC AAC TAC ACC GAT TAC GCT GTG Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val 195 200 205	624
CGC TGG TAC AAT ACC GGC CTG GAA CGC GTG TGG GGC CCA GAT TCC CGC Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 210 215 220	672
GAT TGG GTG AGG TAC AAT CAA TTT CGC CGC GAA CTG ACC CTG ACC GTG Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 225 230 235 240	720
CTC GAT ATC GTG GCT CTG TTC CCA AAT TAC GAT AGC CGC CGC TAC CCA Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro 245 250 255	768

ATT CGA ACC GTG TCC CAA CTG ACC CGC GAA ATT TAC ACC AAC CCA GTG	816
Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val	
260 265 270	
CTG GAA AAT TTT GAT GGT AGC TTT CGC GGC TCC GCT CAG GGC ATC GAA	864
Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu	
275 280 285	
CGC AGC ATT AGG AGC CCA CAT CTG ATG GAT ATC CTG AAC AGC ATC ACC	912
Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr	
290 295 300	
ATC TAC ACC GAT GCT CAT AGG GGT TAC TAC TAC TGG TCC GGC CAT CAA	960
Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Tyr Trp Ser Gly His Gln	
305 310 315 320	
ATC ATG GCT TCC CCT GTG GGC TTT TCC GGG CCA GAA TTC ACC TTT CCA	1008
Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro	
325 330 335	
CTG TAC GGC ACG ATG GGC AAT GCC GCT CCA CAA CAA CGC ATT GTG GCT	1056
Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala	
340 345 350	
CAA CTG GGT CAG GGC GTG TAC CGC ACC CTG TCC TCC ACC CTG TAC CGC	1104
Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg	
355 360 365	
CGC CCT TTT AAT ATC GGC ATC AAC AAC CAG CAA CTG TCC GTG CTG GAC	1152
Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp	
370 375 380	
GGC ACC GAA TTT GCT TAC GGC ACC TCC TCC AAT CTG CCA TCC GCT GTA	1200
Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val	
385 390 395 400	
TAC CGC AAG AGC GGC ACC GTG GAT TCC CTG GAT GAA ATC CCA CCA CAG	1248
Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln	
405 410 415	
AAT AAC AAC GTG CCA CCT AGG CAA GGC TTT AGC CAT CGC CTG AGC CAT	1296
Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His	
420 425 430	
GTG TCC ATG TTT CGC TCC GGC TTT AGC AAT AGC AGC GTG AGC ATC ATC	1344
Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile	
435 440 445	
CGC GCT CCT ATG TTC TCC TGG ATC CAC CGC TCC GCT GAG TTC AAC AAC	1392
Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn	
450 455 460	
ATC ATC CCG TCC TCC CAA ATC ACC CAA ATC CCG CTC ACC AAG TCC ACG	1440
Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr	
465 470 475 480	
AAC CTC GGC TCC GGC ACG TCC GTC GTC AAG GGC CCG GGC TTC ACC GGC	1488
Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly	
485 490 495	

GGC GAC ATC CTC CGC CGC ACG TCC CCG GGC CAG ATC TCC ACC CTC CGC	1536
Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg	
500 505 510	
GTC AAC ATC ACG GCT CCG CTG AGC CAG CGC TAC AGG GTG CGC ATC AGA	1584
Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg	
515 520 525	
TAC GCT AGC ACG ACC AAC CTG CAA TTC CAC ACG TCC ATC GAC GGC AGA	1632
Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg	
530 535 540	
CCG ATC AAC CAG GGC AAC TTC AGC GCG ACG ATG AGC TCC GGG TCC AAC	1680
Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn	
545 550 555 560	
CTC CAG TCC GGC TCC TTC CGC ACG GTC GGT TTC ACC ACG CCG TTC AAC	1728
Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn	
565 570 575	
TTC TCC AAC GGC TCC TCC GTC TTC ACG CTC TCC GCT CAC GTC TTC AAC	1776
Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn	
580 585 590	
TCC GGC AAC GAG GTG TAC ATC GAC CGC ATC GAG TTC GTC CCG GCC GAG	1824
Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu	
595 600 605	
GTC ACC TTC GAG CTC GAG TAGGTA	1848
Val Thr Phe Glu Leu Glu	
610	

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 614 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu	
1 5 10 15	
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly	
20 25 30	
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser	
35 40 45	
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile	
50 55 60	
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile	
65 70 75 80	
Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala	
85 90 95	

Ile	Ser	Arg	Leu	Glu	Gly	Leu	Ser	Asn	Leu	Tyr	Gln	Ile	Tyr	Ala	Glu	100	105	110
Ser	Phe	Arg	Glu	Trp	Glu	Ala	Asp	Pro	Thr	Asn	Pro	Ala	Leu	Arg	Glu	115	120	125
Glu	Met	Arg	Ile	Gln	Phe	Asn	Asp	Met	Asn	Ser	Ala	Leu	Thr	Thr	Ala	130	135	140
Ile	Pro	Leu	Phe	Ala	Val	Gln	Asn	Tyr	Gln	Val	Pro	Leu	Leu	Ser	Val	145	150	155
Tyr	Val	Gln	Ala	Ala	Asn	Leu	His	Leu	Ser	Val	Leu	Arg	Asp	Val	Ser	165	170	175
Val	Phe	Gly	Gln	Arg	Trp	Gly	Phe	Asp	Ala	Ala	Thr	Ile	Asn	Ser	Arg	180	185	190
Tyr	Asn	Asp	Leu	Thr	Arg	Leu	Ile	Gly	Asn	Tyr	Thr	Asp	Tyr	Ala	Val	195	200	205
Arg	Trp	Tyr	Asn	Thr	Gly	Leu	Glu	Arg	Val	Trp	Gly	Pro	Asp	Ser	Arg	210	215	220
Asp	Trp	Val	Arg	Tyr	Asn	Gln	Phe	Arg	Arg	Glu	Leu	Thr	Leu	Thr	Val	225	230	235
Leu	Asp	Ile	Val	Ala	Leu	Phe	Pro	Asn	Tyr	Asp	Ser	Arg	Arg	Tyr	Pro	245	250	255
Ile	Arg	Thr	Val	Ser	Gln	Leu	Thr	Arg	Glu	Ile	Tyr	Thr	Asn	Pro	Val	260	265	270
Leu	Glu	Asn	Phe	Asp	Gly	Ser	Phe	Arg	Gly	Ser	Ala	Gln	Gly	Ile	Glu	275	280	285
Arg	Ser	Ile	Arg	Ser	Pro	His	Leu	Met	Asp	Ile	Leu	Asn	Ser	Ile	Thr	290	295	300
Ile	Tyr	Thr	Asp	Ala	His	Arg	Gly	Tyr	Tyr	Tyr	Trp	Ser	Gly	His	Gln	305	310	315
Ile	Met	Ala	Ser	Pro	Val	Gly	Phe	Ser	Gly	Pro	Glu	Phe	Thr	Phe	Pro	325	330	335
Leu	Tyr	Gly	Thr	Met	Gly	Asn	Ala	Ala	Pro	Gln	Gln	Arg	Ile	Val	Ala	340	345	350
Gln	Leu	Gly	Gln	Gly	Val	Tyr	Arg	Thr	Leu	Ser	Ser	Thr	Leu	Tyr	Arg	355	360	365
Arg	Pro	Phe	Asn	Ile	Gly	Ile	Asn	Asn	Gln	Gln	Leu	Ser	Val	Leu	Asp	370	375	380
Gly	Thr	Glu	Phe	Ala	Tyr	Gly	Thr	Ser	Ser	Asn	Leu	Pro	Ser	Ala	Val	385	390	395
Tyr	Arg	Lys	Ser	Gly	Thr	Val	Asp	Ser	Leu	Asp	Glu	Ile	Pro	Pro	Gln	405	410	415
Asn	Asn	Asn	Val	Pro	Pro	Arg	Gln	Gly	Phe	Ser	His	Arg	Leu	Ser	His	420	425	430

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
 435 440 445
 Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
 450 455 460
 Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr
 465 470 475 480
 Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly
 485 490 495
 Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg
 500 505 510
 Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg
 515 520 525
 Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg
 530 535 540
 Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn
 545 550 555 560
 Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn
 565 570 575
 Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn
 580 585 590
 Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu
 595 600 605
 Val Thr Phe Glu Leu Glu
 610

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 185 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGCTTGCAGC GAGTACATAC ATACTAGGCA GCCAGGCAGC CATGGCGCCC ACCGTGATGA	60
TGGCCTCGTC GGCCACCGCC GTCGCTCCGT TCCAGGGGCT CAAGTCCACC GCCAGCCTCC	120
CCGTCGCCCCG CCGGTCCTCC AGAAGCCTCG GCAACGTCAG CAACGGCGGA AGGATCCGGT	180
GCATG	185

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 177 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ACGTCGCTCA TGTATGTATG ATCCGTCGGT CCGTCGGTAC CGCGGGTGGC ACTACTACCG	60
GAGCAGCCGG TGGCGGCAGC GAGGCAAGGT CCCCAGATTG AGGTGGCGGT CGGAGGGGCA	120
GCGGGCGGCC AGGAGGTCTT CGGAGCCGTT GCAGTCGTTG CCGCCTTCCT AGGCCAC	177

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATCACTTTCA CGGGA	15
------------------	----

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATCACGTTCA CGGCA	15
------------------	----

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ile Thr Phe Thr Gly
1 5

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCTTGGCAGC CATCACGTTT ACGGGAAGTA TTGTC	35
--	----

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCTGGCAGC AGAAAAACAA GTAGTTGAGA ACTAAGAAGA AGAAA

45

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CATCGAGACA AGCACGGTCA ACTTC

25

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AAGTCCCTGG AGGCACAGGG CTTCAAGA

28

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCTTACCTAC TAATTGTTCT TGG

23

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CAGGGTACAT ATTTGCCTTG GG

22

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AACCCTGAAT GGAAGTGC

18

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ACGGACAGAT GCAGATTGG

19